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RAW SEQUENCE LISTING   DATE: 01/23/2002
PATENT APPLICATION: US/09/865,363   TIME: 09:53:48

Input Set : **N:\Crf3\RULE60\09865363.raw.txt**
Output Set: **N:\CRF3\01232002\I865363.raw**

SEQUENCE LISTING

```
 3  (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Anderson, Dirk M.
 6                     Galibert, Laurent
 7                     Maraskovsky, Eugene
 9     (ii) TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
11    (iii) NUMBER OF SEQUENCES: 19
13     (iv) CORRESPONDENCE ADDRESS:
14          (A) ADDRESSEE: Immunex Corporation, Law Department
15          (B) STREET: 51 University Street
16          (C) CITY: Seattle
17          (D) STATE: WA
18          (E) COUNTRY: USA
19          (F) ZIP: 98101
21      (v) COMPUTER READABLE FORM:
22          (A) MEDIUM TYPE: Floppy disk
23          (B) COMPUTER: Apple Power Macintosh
24          (C) OPERATING SYSTEM: Apple Operating System 7.5.5
25          (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
27     (vi) CURRENT APPLICATION DATA:
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C--> 28   **(A) APPLICATION NUMBER: US/09/865,363**
C--> 29   **(B) FILING DATE: 25-May-2001**
```
45          (C) CLASSIFICATION:
42    (vii) PRIOR APPLICATION DATA:
33          (A) APPLICATION NUMBER: 08/995,659
34          (B) FILING DATE:
38          (A) APPLICATION NUMBER: USSN 08/813,509
39          (B) FILING DATE: 07 MARCH 1997
43          (A) APPLICATION NUMBER: USSN 08/772,330
44          (B) FILING DATE: 23 DECEMBER 1996
47   (viii) ATTORNEY/AGENT INFORMATION:
48          (A) NAME: Perkins, Patricia Anne
49          (B) REGISTRATION NUMBER: 34,693
50          (C) REFERENCE/DOCKET NUMBER: 2852-A
52     (ix) TELECOMMUNICATION INFORMATION:
53          (A) TELEPHONE: (206)587-0430
54          (B) TELEFAX: (206)233-0644
57  (2) INFORMATION FOR SEQ ID NO: 1:
59      (i) SEQUENCE CHARACTERISTICS:
60          (A) LENGTH: 3115 base pairs
61          (B) TYPE: nucleic acid
62          (C) STRANDEDNESS: single
63          (D) TOPOLOGY: linear
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65     (ii) MOLECULE TYPE: cDNA
67    (iii) HYPOTHETICAL: NO
69     (iv) ANTI-SENSE: NO
71     (vi) ORIGINAL SOURCE:
72          (A) ORGANISM: HOMO SAPIENS
74    (vii) IMMEDIATE SOURCE:
75          (A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
76          (B) CLONE: 9D-8A
78     (ix) FEATURE:
79          (A) NAME/KEY: CDS
80          (B) LOCATION: 93..1868
83     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
85 GCTGCTGCTG CTCTGCGCGC TGCTCGCCCG GCTGCAGTTT TATCCAGAAA GAGCTGTGTG      60
87 GACTCTCTGC CTGACCTCAG TGTTCTTTTC AG GTG GCT TTG CAG ATC GCT CCT      113
88                                     Val Ala Leu Gln Ile Ala Pro
89                                      1                   5
91 CCA TGT ACC AGT GAG AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC      161
92 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
93          10              15                  20
95 AAA TGT GAA CCA GGA AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT      209
96 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
97      25                  30                  35
99 GAC AGT GTA TGT CTG CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG      257
100 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
101 40                  45                  50                  55
103 AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG      305
104 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
105                 60                  65                  70
107 GCC CTG GTG GCC GTG GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC      353
108 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
109             75                  80                  85
111 GCG TGC ACG GCT GGG TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC      401
112 Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
113         90                  95                  100
115 CGC AAC ACC GAG TGC GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG      449
116 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
117     105                 110                 115
119 CTC AAC AAG GAC ACA GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT      497
120 Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
121 120                 125                 130                 135
123 GAT GCC TTT TCC TCC ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC      545
124 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
125             140                 145                 150
127 TTC CTT GGA AAG AGA GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG      593
128 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
129             155                 160                 165
131 GTT TGC AGT TCT TCT CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT      641
132 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
133         170                 175                 180
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```
135 GTT TAC TTG CCC GGT TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC          689
136 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala
137     185                 190                 195
139 CTG GTG GCT GCC ATC ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA          737
140 Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys
141 200                 205                 210                 215
143 GCA CTC ACA GCT AAT TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC CGC          785
144 Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
145                 220                 225                 230
147 CTA AGT GGA GAT AAG GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC          833
148 Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His
149                 235                 240                 245
151 ACG GCA AAC TTT GGT CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG          881
152 Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu
153                 250                 255                 260
155 ACT CTG GAG GAG AAG ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA          929
156 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln
157     265                 270                 275
159 GGT GGT GTC TGT CAG GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA          977
160 Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln
161 280                 285                 290                 295
163 GGC GAA GAT GCC AGG ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG         1025
164 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu
165                 300                 305                 310
167 GAA GAC AGC TTC AGA CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG         1073
168 Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
169                 315                 320                 325
171 CCC TCC CAG CCC ACA GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC         1121
172 Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
173                 330                 335                 340
175 AAA TCC ACA CCT CCT TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC         1169
176 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
177     345                 350                 355
179 AGT TTA AGC CAG TGC TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA         1217
180 Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
181 360                 365                 370                 375
183 AGC TGC AAC TGC ACT GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG         1265
184 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
185                 380                 385                 390
187 TCC TCT GAA AAC TAC TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG         1313
188 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
189                 395                 400                 405
191 CAC TGG GCA GCC AGC CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC         1361
192 His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly
193                 410                 415                 420
195 TGC CGG AAC CCT CCT GGG GAG GAC TGT GAA CCC CTC GTG GGT TCC CCA         1409
196 Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro
197     425                 430                 435
199 AAA CGT GGA CCC TTG CCC CAG TGC GCC TAT GGC ATG GGC CTT CCC CCT         1457
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200 Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro
201 440             445             450             455
203 GAA GAA GAA GCC AGC AGG ACG GAG GCC AGA GAC CAG CCC GAG GAT GGG      1505
204 Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly
205             460             465             470
207 GCT GAT GGG AGG CTC CCA AGC TCA GCG AGG GCA GGT GCC GGG TCT GGA      1553
208 Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly
209             475             480             485
211 AGC TCC CCT GGT GGC CAG TCC CCT GCA TCT GGA AAT GTG ACT GGA AAC      1601
212 Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn
213         490             495             500
215 AGT AAC TCC ACG TTC ATC TCC AGC GGG CAG GTG ATG AAC TTC AAG GGC      1649
216 Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly
217     505             510             515
219 GAC ATC ATC GTG GTC TAC GTC AGC CAG ACC TCG CAG GAG GGC GCG GCG      1697
220 Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala
221 520             525             530             535
223 GCG GCT GCG GAG CCC ATG GGC CGC CCG GTG CAG GAG GAG ACC CTG GCG      1745
224 Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala
225             540             545             550
227 CGC CGA GAC TCC TTC GCG GGG AAC GGC CCG CGC TTC CCG GAC CCG TGC      1793
228 Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys
229             555             560             565
231 GGC GGC CCC GAG GGG CTG CGG GAG CCG GAG AAG GCC TCG AGG CCG GTG      1841
232 Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val
233         570             575             580
235 CAG GAG CAA GGC GGG GCC AAG GCT TGA GCGCCCCCA TGGCTGGGAG           1888
236 Gln Glu Gln Gly Gly Ala Lys Ala
237     585             590
239 CCCGAAGCTC GGAGCCAGGG CTCGCGAGGG CAGCACCGCA GCCTCTGCCC CAGCCCCGGC  1948
241 CACCCAGGGA TCGATCGGTA CAGTCGAGGA AGACCACCCG GCATTCTCTG CCCACTTTGC  2008
243 CTTCCAGGAA ATGGGCTTTT CAGGAAGTGA ATTGATGAGG ACTGTCCCCA TGCCCACGGA  2068
245 TGCTCAGCAG CCCGCCGCAC TGGGGCAGAT GTCTCCCCTG CCACTCCTCA AACTCGCAGC  2128
247 AGTAATTTGT GGCACTATGA CAGCTATTTT TATGACTATC CTGTTCTGTG GGGGGGGGGT  2188
249 CTATGTTTTC CCCCCATATT TGTATTCCTT TTCATAACTT TTCTTGATAT CTTTCCTCCC  2248
251 TCTTTTTTAA TGTAAAGGTT TTCTCAAAAA TTCTCCTAAA GGTGAGGGTC TCTTTCTTTT  2308
253 CTCTTTTCCT TTTTTTTTTC TTTTTTTGGC AACCTGGCTC TGGCCCAGGC TAGAGTGCAG  2368
255 TGGTGCGATT ATAGCCCGGT GCAGCCTCTA ACTCCTGGGC TCAAGCAATC CAAGTGATCC  2428
257 TCCCACCTCA ACCTTCGGAG TAGCTGGGAT CACAGCTGCA GGCCACGCCC AGCTTCCTCC  2488
259 CCCCGACTCC CCCCCCCCAG AGACACGGTC CCACCATGTT ACCCAGCCTG GTCTCAAACT  2548
261 CCCCAGCTAA AGCAGTCCTC CAGCCTCGGC CTCCCAAAGT ACTGGGATTA CAGGCGTGAG  2608
263 CCCCCACGCT GGCCTGCTTT ACGTATTTTC TTTTGTGCCC CTGCTCACAG TGTTTTAGAG  2668
265 ATGGCTTTCC CAGTGTGTGT TCATTGTAAA CACTTTTGGG AAAGGGCTAA ACATGTGAGG  2728
267 CCTGGAGATA GTTGCTAAGT TGCTAGGAAC ATGTGGTGGG ACTTTCATAT TCTGAAAAAT  2788
269 GTTCTATATT CTCATTTTTC TAAAAGAAAG AAAAAAGGAA ACCCGATTTA TTTCTCCTGA  2848
271 ATCTTTTTAA GTTTGTGTCG TTCCTTAAGC AGAACTAAGC TCAGTATGTG ACCTTACCCG  2908
273 CTAGGTGGTT AATTTATCCA TGCTGGCAGA GGCACTCAGG TACTTGGTAA GCAAATTTCT  2968
275 AAAACTCCAA GTTGCTGCAG CTTGGCATTC TTCTTATTCT AGAGGTCTCT CTGGAAAAGA  3028
277 TGGAGAAAAT GAACAGGACA TGGGGCTCCT GGAAAGAAAG GGCCCGGGAA GTTCAAGGAA  3088
```

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```
279 GAATAAAGTT GAAATTTTAA AAAAAAA                                          3115
282 (2) INFORMATION FOR SEQ ID NO: 2:
284      (i) SEQUENCE CHARACTERISTICS:
285          (A) LENGTH: 591 amino acids
286          (B) TYPE: amino acid
287          (D) TOPOLOGY: linear
289     (ii) MOLECULE TYPE: protein
291     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
293 Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu
294  1               5                  10                  15
296 His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser
297              20                  25                  30
299 Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro
300              35                  40                  45
302 Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys Leu Leu His
303         50                  55                  60
305 Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Ala Gly Asn
306  65                  70                  75                  80
308 Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser
309                  85                  90                  95
311 Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu
312              100                 105                 110
314 Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro
315              115                 120                 125
317 Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys
318         130                 135                 140
320 Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His
321 145                 150                 155                 160
323 Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg
324              165                 170                 175
326 Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu
327              180                 185                 190
329 Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val
330              195                 200                 205
332 Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp
333         210                 215                 220
335 Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly
336 225                 230                 235                 240
338 Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala
339              245                 250                 255
341 Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu
342              260                 265                 270
344 Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly Thr Cys Val
345         275                 280                 285
347 Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu
348         290                 295                 300
350 Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr
351 305                 310                 315                 320
353 Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu
```

VERIFICATION SUMMARY   DATE: 01/23/2002
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Input Set : N:\Crf3\RULE60\09865363.raw.txt
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:440 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:445 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:453 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:463 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:469 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:473 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:487 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:528 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:533 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:537 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:551 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:555 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:561 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

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Output Set: **N:\CRF3\01232002\I865363.raw**

L:565 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:566 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3